STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: _10/574,018A_

Source: _1FWO_

Date Processed by STIC: _12/5/06_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u>
<u>VERSION 4.4.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
    http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio **(<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission
   User Manual - ePAVE)**
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street,
   Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/574,018A_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
   Wrapped Aminos   was retrieved in a word processor **after** creating it. Please adjust your right margin to .3; this will
   prevent "wrapping."

2 ____Invalid Line Length   The rules require that a line **not exceed 72 characters** in length. This includes white spaces.

3 ✓ Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do **not** use tab codes between numbers;
   Numbering   use **space characters**, instead.

4 ____Non-ASCII   The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please
   ensure your subsequent submission is saved in ASCII text.**

5 ____Variable Length   Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules,
   each n or Xaa can only represent a single residue.** Please present the **maximum** number of each
   residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
   "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
   previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
   the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for
   Artificial or Unknown sequences.**

7 ____Skipped Sequences   Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence:
   (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
   (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
   (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
   This sequence is intentionally skipped
   Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.

8 ____Skipped Sequences   Sequence(s) _____ missing. If **intentional**, please insert the following lines for **each** skipped sequence.
   (NEW RULES)   <210> sequence id number
   <400> sequence id number
   000

9 ____Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
   (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
   In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____Invalid <213>   Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or
   Response   scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or
   is Artificial Sequence. (see item 11 below)

11 ____Use of <220>   Sequence(s) ___ missing the <220> "Feature" and associated numeric identifiers and responses. Use
   of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown."
   Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as
   explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of
   Sequence Rules

12 ____PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
   "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
   listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n/Xaa   "n" can **only** represent a single <u>nucleotide</u>; "Xaa" can **only** represent a single <u>amino acid</u>

AMC – STIC Systems Branch – 03/02/06

RAW SEQUENCE LISTING
PATENT APPLICATION: **US/10/574,018A**

DATE: 12/05/2006
TIME: 10:04:55

Input Set : **N:\RJAVED\10574018A.txt**
Output Set: **N:\CRF4\12052006\J574018A.raw**

```
   3 <110> APPLICANT: The Hospital for Sick Children
   5 <120> TITLE OF INVENTION: Method of in situ Detection of Proteins Using
   6       Aptamers
   8 <130> FILE REFERENCE: 3206-276 LAB
  10 <140> CURRENT APPLICATION NUMBER: 10/574,018A
C--> 11 <141> CURRENT FILING DATE: 2006-03-29
  14 <150> PRIOR APPLICATION NUMBER: U.S. 60/506776
  15 <151> PRIOR FILING DATE: 2003-09-30
  17 <160> NUMBER OF SEQ ID NOS: 9
  19 <170> SOFTWARE: PatentIn Ver. 3.1
```

see pp 1-2

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

```
  50 <210> SEQ ID NO: 3
  51 <211> LENGTH: 12
  52 <212> TYPE: PRT
  53 <213> ORGANISM: (Peptide)
  55 <400> SEQUENCE: 3
  57 Met Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Gly
E-->58 1            5                    10
  61 <210> SEQ ID NO: 4
  62 <211> LENGTH: 73
  63 <212> TYPE: DNA
  64 <213> ORGANISM: Artificial
  66 <220> FEATURE:
  67 <223> OTHER INFORMATION: Primer
  69 <400> SEQUENCE: 4
E-->71 gggtttttaag cttaccatgg gatatcccta tgatgtgcca gactacgcgg gaatgtctag 60  attagataaa
E-->72 agt                                                       73
```

invalid response. See item 10 on Error Summary Sheet

misaligned numbering. See item 3 on Error Summary Sheet.

insert a hard return

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 12/05/2006
PATENT APPLICATION: US/10/574,018A   TIME: 10:04:56

FyI

Input Set : **N:\RJAVED\10574018A.txt**
Output Set: **N:\CRF4\12052006\J574018A.raw**

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:4; Line(s) 71

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823 (b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,4,5,6,7,8,9

VERIFICATION SUMMARY   DATE: 12/05/2006
PATENT APPLICATION: **US/10/574,018A**   TIME: 10:04:56

Input Set : **N:\RJAVED\10574018A.txt**
Output Set: **N:\CRF4\12052006\J574018A.raw**

L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:58 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
L:71 M:334 E: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:8
L:72 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:4
L:72 M:254 E: No. of Bases conflict, LENGTH:Input:73 Counted:3 SEQ:4
L:72 M:252 E: No. of Seq. differs, <211> LENGTH:Input:73 Found:3 SEQ:4